

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/978,343DATE: 01/17/2002  
TIME: 21:39:40

INPUT SET: S36724.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: HOSTETTER, MARGARET K.  
GALE, CHERYL A.  
BENDEL, CATHERINE M.  
TAO, NIAN-JUN  
KENDRICK, KATHLEEN

**ENTERED**

(ii) TITLE OF INVENTION: CANDIDA ALBICANS GENE, INTEGRIN-LIKE  
PROTEIN, ANTIBODIES, AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 12

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.  
(B) STREET: 119 NORTH FOURTH STREET, SUITE 203  
(C) CITY: MINNEAPOLIS  
(D) STATE: MINNESOTA  
(E) COUNTRY: USA  
(F) ZIP: 55401

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/978,343  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/642,846  
(B) FILING DATE: 03-MAY-1996

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MUETING, ANN M.  
(B) REGISTRATION NUMBER: 33,977  
(C) REFERENCE/DOCKET NUMBER: 110.00280101

## (ix) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: 612-305-1217  
48 (B) TELEFAX: 612-305-1228  
49  
50

51 (2) INFORMATION FOR SEQ ID NO:1:  
52

53 (i) SEQUENCE CHARACTERISTICS:  
54 (A) LENGTH: 5194 base pairs  
55 (B) TYPE: nucleic acid  
56 (C) STRANDEDNESS: single  
57 (D) TOPOLOGY: linear  
58

59 (ii) MOLECULE TYPE: DNA (genomic)  
60  
61  
62  
63

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
65

66	CCCAAAAAG ATAAAATAAA AACAAAACAA AACAAAAGTA CTAACAAATT ATTGAACTT	60
67		
68	TTAATTTTTA ATAAAGAATC AGTAGATCTA TTGTTAAAAG AAATGAACTC AACTCCAAGT	120
69		
70	AAATTATTAC CGATAGATAA ACATTCTCAT TTACAATTAC AGCCTCAATC GTCCTCGGCA	180
71		
72	TCAATATTTA ATTCCCCAAC AAAACCATTG AATTTCCCCA GAACAAATTC CAAGCCGAGT	240
73		
74	TTAGATCCAA ATTCAAGCTC TGATACCTAC ACTAGCGAAC AAGATCAAGA GAAAGGGAAA	300
75		
76	GAAGAGAAAA AGGACACAGC CTTTCAAACA TCTTTTGATA GAAATTTTGA TCTTGATAAT	360
77		
78	TCAATCGATA TACAACAAAC AATTCAACAT CAGCAACAAC AGCCACAACA ACAACAACAA	420
79		
80	CTCTCACAAA CCGACAATAA TTTAATTGAT GAATTTTCTT TTCAAACACC GATGACTTCG	480
81		
82	ACTTTAGACC TAACCAAGCA AAATCCAACT GTGGACAAAG TGAATGAAAA TCATGCACCA	540
83		
84	ACTTATATAA ATACCTCCCC CAACAAATCA ATAATGAAAA AGGCAACTCC TAAAGCGTCA	600
85		
86	CCTAAAAAAG TTGCATTTAC TGTAACATAAT CCCGAAATTC ATCATTATCC AGATAATAGA	660
87		
88	GTCGAGGAAG AAGATCAAAG TCAACAAAAA GAAGATTCAG TTGAGCCACC CTTAATACAA	720
89		
90	CATCAATGGA AAGATCCTTC TCAATTCAAT TATTCTGATG AAGATACAAA TGCTTCAGTT	780
91		
92	CCACCAACAC CACCACTTCA TACGACGAAA CCTACTTTTG CGCAATTATT GAACAAAAAC	840
93		
94	AACGAAGTCA ATCTGGAACC AGAGGCATTG ACAGATATGA AATTAAAGCG CGAAAATTC	900
95		
96	AGCAATTTAT CATTAGATGA AAAAGTCAAT TTATATCTTA GTCCCACTAA TAATAACAAT	960
97		
98	AGTAAGAATG TGTCAGATAT GGATCTGCAT TTACAAAAC TGCAAGACGC TTCGAAAAAC	1020
99		

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100	AAACTAATG	AAAATATTCA	CAATTTGTCA	TTTGCTTTAA	AAGCACCAAA	GAATGATATT	1080
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102	GAAAACCCAT	TAAACTCATT	GACTAACGCA	GATATTCTGT	TAAGATCATC	TGGATCATCA	1140
103							
104	CAATCGTCAT	TACAATCTTT	GAGGAATGAC	AATCGTGTCT	TGGAATCAGT	GCCTGGGTCA	1200
105							
106	CCTAAGAAGG	TTAATCCTGG	ATTGTCTTTG	AATGACGGCA	TAAAGGGGTT	CTCTGATGAG	1260
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108	GTTGTTGAAT	CATTACTTCC	TCGTGACTTA	TCTCGAGACA	AATTAGAGAC	TACAAAAGAA	1320
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110	CATGATGCAC	CAGAACACAA	CAATGAGAAT	TTTATTGATG	CTAAATCGAC	TAATACCAAT	1380
111							
112	AAGGGACAAC	TCTTAGTATC	ATCTGATGAT	CATTTGGACT	CTTTTGATAG	ATCCTATAAC	1440
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114	CACACTGAAC	AATCAATTTT	GAATCTTTTG	AATAGTGCAT	CACAATCTCA	AATTTCTGTTA	1500
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116	AATGCATTGG	AAAAACAAAG	GCAAACACAG	GAACAAGAAC	AAACACAAGC	GGCAGAGCCT	1560
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118	GAAGAAGAAA	CTTCGTTTAG	TGATAATATC	AAAGTTAAAC	AAGAGCCAAA	GAGCAATTTG	1620
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121							
122	AAAAGAGAAT	TTTCAAGTCG	AATATTAAGA	ATAAAAAATG	AAGATGAAAT	TGCCGAACCA	1740
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128	ATGTCAATTC	GTTTTTCATAT	TGATAGTGAT	TGGAAATTGG	AAGACAGTAA	TGATGGCGAT	1920
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130	AGAGAAGATA	ATGATGATAT	TTCTCGTTTT	GAGAAATCAG	ATATTTTGAA	CGACGTATCA	1980
131							
132	CAGACTTCTG	ATATTATTGG	TGACAAATAT	GGAACTCAT	CAAGTGAAAT	AACCACCAAA	2040
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134	ACATTAGCAC	CCCCAAGATC	GGACAACAAT	GACAAGGAGA	ATTCTAAATC	TTTGGAAGAT	2100
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136	CCAGCTAATA	ATGAATCATT	GCAACAACAA	TTGGAGGTAC	CGCATACAAA	AGAAGATGAT	2160
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138	AGCATTTTAG	CCAATCGTC	CAATATTGCT	CCACCTGAAG	AATTGACTTT	GCCCGTAGTG	2220
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140	GAAGCAAATG	ATTATTCATC	TTTTAATGAC	GTGACCAAAA	CTTTTGATGC	ATACTCAAGC	2280
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142	TTTGAAGAGT	CATTATCTAG	AGAGCACGAA	ACTGATTCAA	AACCAATTAA	TTTCATATCA	2340
143							
144	ATTTGGCATA	AACAAGAAAA	GCAGAAGAAA	CATCAAATTC	ATAAAGTTCC	AACTAAACAG	2400
145							
146	ATCATTGCTA	GTTATCAACA	ATACAAAAAC	GAACAAGAAT	CTCGTGTTAC	TAGTGATAAA	2460
147							
148	GTGAAAATCC	CAAATGCCAT	ACAATTCAAG	AAATTCAAAG	AGGTAAATGT	CATGTCAAGA	2520
149							
150	AGAGTTGTTA	GTCCAGACAT	GGATGATTTG	AATGTATCTC	AATTTTTTACC	AGAATTATCT	2580
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152	GAAGACTCTG	GATTTAAAGA	TTTGAATTTT	GCCAACTACT	CCAATAACAC	CAACAGACCA	2640

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154	AGAAGTTTTA	CTCCATTGAG	CACTAAAAAT	GTCTTGTCGA	ATATTGATAA	CGATCCTAAT	2700
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157							
158	GCTAATAAGG	CAGCGCCAAA	TCAGGCACCA	CCATTGCCAC	CACAACGACA	ACCATCTTCA	2820
159							
160	ACTCGTTCCA	ATTCAAATAA	ACGAGTGTCC	AGATTTAGAG	TGCCCACATT	TGAAATTAGA	2880
161							
162	AGAACTTCTT	CAGCATTAGC	ACCTTGTGAC	ATGTATAATG	ATATTTTTGA	TGATTTCTGGT	2940
163							
164	GCGGGTTCTA	AACCAACTAT	AAAGGCAGAA	GGAATGAAAA	CATTGCCAAG	TATGGATAAA	3000
165							
166	GATGATGTCA	AGAGGATTTT	GAATGCAAAG	AAAGGTGTGA	CTCAAGATGA	ATATATAAAT	3060
167							
168	GCCAAACTTG	TTGATCAAAA	ACCTAAAAAG	AATTCAATTG	TCACCGATCC	CGAAGACCGA	3120
169							
170	TATGAAGAAT	TACAACAAAC	TGCCTCTATA	CACAATGCCA	CCATTGATTC	AAGTATTTAT	3180
171							
172	GGCCGACCAG	ACTCCATTTT	TACCGACATG	TTGCCTTATC	TTAGTGATGA	ATTGAAAAAA	3240
173							
174	CCACCTACGG	CTTTATTATC	TGCTGATCGT	TTGTTTATGG	AACAAGAAGT	ACATCCGTTA	3300
175							
176	AGATCAAAC	CTGTTTTGGT	TCACCCAGGG	GCAGGAGCAG	CAACTAATTC	TTCAATGTTA	3360
177							
178	CCAGAGCCAG	ATTTTGAATT	AATCAATTCA	CCTGCTAGAA	ATGTGCTGAA	CAACAGTGAT	3420
179							
180	AATGTCGCCA	TCAGTGGTAA	TGCTAGTACT	ATTAGTTTTA	ACCAATTGGA	TATGAATTTT	3480
181							
182	GATGACCAAG	CTACAATTGG	TCAAAAAATC	CAAGAGCAAC	CTGCTTCAAA	ATCCGCCAAT	3540
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184	ACTGTTCTGT	GTGATGATGA	TGGATTGGCC	AGTGCACCTG	AAACACCAAG	AACTCCTACC	3600
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186	AAAAAGGAGT	CCATATCAAG	CAAGCCTGCC	AAGCTTTCTT	CTGCCTCCCC	TAGAAAATCA	3660
187							
188	CCAATTAAGA	TTGGTTCACC	AGTTCGAGTT	ATTAAGAAAA	ATGGATCAAT	TGCTGGCATT	3720
189							
190	GAACCAATCC	CAAAAGCCAC	TCACAAACCG	AAGAAATCAT	TCCAAGGAAA	CGAGATTTCA	3780
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192	AACCATAAAG	TACGAGATGG	TGGAATTTCA	CCAAGCTCCG	GATCAGAGCA	TCAACAGCAT	3840
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194	AATCCTAGTA	TGGTTTCTGT	TCCTTCACAG	TATACTGATG	CTACTTCAAC	GGTTCCAGAT	3900
195							
196	GAAAACAAAG	ATGTTCAACA	CAAGCCTCGT	GAAAAGCAAA	AGCAAAAGCA	TCACCATCGC	3960
197							
198	CATCATCATC	ATCATCATAA	ACAAAAAACT	GATATTCCGG	GTGTTGTTGA	TGATGAAATT	4020
199							
200	CCTGATGTAG	GATTACAAGA	ACGAGGCAAA	TTATTCTTTA	GAGTTTTAGG	AATTAAGAAT	4080
201							
202	ATCAATTTAC	CCGATATTAA	TACTCACAAA	GGAAGATTCA	CTTTAACGTT	GGATAATGGA	4140
203							
204	GTGCATTGTG	TTACTACACC	AGAATACAAC	ATGGACGACC	ATAATGTTGC	CATAGGTAAA	4200
205							

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206 GAATTTGAGT TGACAGTTGC TGATTCATTA GAGTTTATTT TAACTTTGAA GGCATCATAT 4260
207
208 GAAAAACCTC GTGGTACATT AGTAGAAGTG ACTGAAAAGA AAGTTGTCAA ATCAAGAAAT 4320
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210 AGATTGAGTC GATTATTTGG ATCGAAAGAT ATTATCACCA CGACAAAGTT TGTGCCCCACT 4380
211
212 GAAGTCAAAG ATACCTGGGC TAATAAGTTT GCTCCTGATG GTTCATTTGC TAGATGTTAC 4440
213
214 ATTGATTTAC AACAATTTGA AGACCAAATC ACCGGTAAAG CATCACAGTT TGATCTCAAT 4500
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216 TGTTTTAATG AATGGGAAAC TATGAGTAAT GGCAATCAAC CAATGAAAAG AGGCAAACCT 4560
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218 TATAAGATTG CTCAATTGGA AGTTAAATG TTGTATGTTT CACGATCAGA TCCAAGAGAA 4620
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220 ATATTACCAA CCAGCATTAG ATCCGCATAT GAAAGCATCA ATGAATTAAA CAATGAACAG 4680
221
222 AATAATTACT TTGAAGGTTA TTTACATCAA GAAGGAGGTG ATTGTCCAAT TTTTAAGAAA 4740
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224 CGTTTTTTCA AATTAATGGG CACTTCTTTA TTGGCTCATA GTGAAATATC TCATAAAACT 4800
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226 AGAGCCAAAA TTAATTTATC AAAAGTTGTT GATTTGATTT ATGTTGATAA AGAAAAACATT 4860
227
228 GATCGTTCCA ATCATCGAAA TTTCAGTGAT GTGTTATTGT TGGATCATGC ATTCAAAATC 4920
229
230 AAATTTGCTA ATGGTGAGTT GATTGATTTT TGTGCTCCTA ATAAACATGA AATGAAAATA 4980
231
232 TGGATTCAAA ATTTACAAGA AATTATCTAT AGAAATCGGT TCAGACGTCA ACCATGGGTA 5040
233
234 AATTTGATGC TTCAACAACA ACAACAACA CAACAACAAC AAAGCTCCCA ACAGTAATTG 5100
235
236 AAAGGTCTAC TTTTGATTTT TTTAATTTTA ATTGGCAAAT ATATGCCCAT TTTGTATTAT 5160
237
238 CTTTTAGTCT AATAGCGTTT TCTTTTTTTC CAGT 5194
239
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1664 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Asn Ser Thr Pro Ser Lys Leu Leu Pro Ile Asp Lys His Ser His
1           5           10           15
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Leu Gln Leu Gln Pro Gln Ser Ser Ser Ala Ser Ile Phe Asn Ser Pro
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**SEQUENCE VERIFICATION REPORT**  
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Original Text

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**SEQUENCE MISSING ITEM REPORT**  
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< < THERE ARE NO ITEMS MISSING > >

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**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/09/978,343**

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